

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/572,027BDATE: 05/06/98
TIME: 12:59:02

INPUT SET: S25565.raw

This Raw Listing contains the General
Information Section and up to the first 6 pages

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: DeBonte, L. et al.

(ii) TITLE OF INVENTION: PLANTS HAVING MUTANT SEQUENCES THAT CONFER
ALTERED FATTY ACID PROFILES

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Richardson P.C., P.A.
(B) STREET: 60 South Sixth Street, Suite 3300
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55402

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM compatible
(C) OPERATING SYSTEM: Windows95
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/572,027
(B) FILING DATE: 14-DEC-1995
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/416,497
(B) FILING DATE: 04-APR-1995
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/170,886
(B) FILING DATE: 21-DEC-1993
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/739,965
(B) FILING DATE: 05-AUG-1991
(C) CLASSIFICATION:

RECEIVED

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Publishing Division
Corres/Allowed Files (09)

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PATENT APPLICATION US/08/572,027BDATE: 05/06/98
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47 (vi) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: US 07/575,542
49 (B) FILING DATE: 30-AUG-1990
50 (C) CLASSIFICATION:
51
52 (viii) ATTORNEY/AGENT INFORMATION:
53 (A) NAME: Ellinger, Mark S.
54 (B) REGISTRATION NUMBER: 34,812
55 (C) REFERENCE/DOCKET NUMBER: A21-535.10
56
57 (ix) TELECOMMUNICATION INFORMATION:
58 (A) TELEPHONE: 612/335-5070
59 (B) TELEFAX: 612/288-9696
60
61 (2) INFORMATION FOR SEQ ID NO:1:
62
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 1155 base pairs
65 (B) TYPE: nucleic acid
66 (C) STRANDEDNESS: single
67 (D) TOPOLOGY: linear
68
69 (ii) MOLECULE TYPE: DNA
70
71 (iii) HYPOTHETICAL: NO
72
73 (iv) ANTI-SENSE: NO
74
75 (vi) ORIGINAL SOURCE:
76 (A) ORGANISM: Brassica napus
77
78 (ix) FEATURE:
79 (D) OTHER INFORMATION: Wild type F form.
80
81
82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
83
84 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT 48
85 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
86 1 5 10 15
87
88 GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96
89 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
90 20 25 30
91
92 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144
93 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
94 35 40 45
95
96 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC 192
97 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
98 50 55 60
99

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100	TGC	TTC	TAC	TAC	NTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT	240
101	Cys	Phe	Tyr	Tyr	Xaa	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
102	65					70					75					80	
103																	
104	CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAA	GGG	TGC	GTC	288
105	Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
106					85					90					95		
107																	
108	CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	GAA	TGC	GGC	CAC	CAC	GCC	TTC	336
109	Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	
110				100					105					110			
111																	
112	AGC	GAC	TAC	CAG	TGG	CTT	GAC	GAC	ACC	GTC	GGT	CTC	ATC	TTC	CAC	TCC	384
113	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	
114			115					120					125				
115																	
116	TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGC	AGC	CAC	432
117	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His	
118		130					135					140					
119																	
120	CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG	480
121	His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
122	145					150				155						160	
123	AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CTC	AAC	AAC	CCT	TTG	528
124	Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	
125				165					170					175			
126																	
127	GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCG	TTG	576
128	Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu	
129			180					185					190				
130																	
131	TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGA	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT	624
132	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg	
133			195				200					205					
134																	
135	TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC	672
136	Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	
137		210					215					220					
138																	
139	CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC	720
140	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	
141	225					230				235						240	
142																	
143	TTC	CGT	TAC	GCC	GCC	GGC	CAG	GGA	GTG	GCC	TCG	ATG	GTC	TGC	TTC	TAC	768
144	Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr	
145				245					250					255			
146																	
147	GGA	GTC	CCG	CTT	CTG	ATT	GTC	AAT	GGT	TTC	CTC	GTG	TTG	ATC	ACT	TAC	816
148	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr	
149			260					265					270				
150																	
151	TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAC	GAT	TCG	TCC	GAG	TGG	864
152	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	

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153          275          280          285
154
155  GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC      912
156  Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
157      290          295          300
158
159  TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT      960
160  Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
161  305          310          315          320
162
163  CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG      1008
164  Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
165      325          330          335
166
167  ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG      1056
168  Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
169      340          345          350
170
171  GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG      1104
172  Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
173      355          360          365
174
175  GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T      1153
176  Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
177      370          375          380
178
179  GA      1155
180
181
182  (2) INFORMATION FOR SEQ ID NO:2:
183
184      (i) SEQUENCE CHARACTERISTICS:
185          (A) LENGTH: 384 amino acids
186          (B) TYPE: amino acid
187          (D) TOPOLOGY: linear
188
189      (ii) MOLECULE TYPE: protein
190
191      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
192
193  Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
194      1          5          10          15
195
196  Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
197      20          25          30
198
199  Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
200      35          40          45
201
202  Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
203      50          55          60
204
205  Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

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206	65		70		75		80
207							
208	Leu Ser Tyr Phe	Ala Trp Pro Leu Tyr Trp	Ala Cys Gln Gly Cys Val				
209		85	90	95			
210							
211	Leu Thr Gly Val	Trp Val Ile Ala His Glu Cys Gly His His Ala Phe					
212		100	105	110			
213							
214	Ser Asp Tyr Gln	Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser					
215		115	120	125			
216							
217	Phe Leu Leu Val	Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His					
218		130	135	140			
219							
220	His Ser Asn Thr	Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys					
221		145	150	155	160		
222							
223	Lys Lys Ser Asp	Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu					
224		165	170	175			
225							
226	Gly Arg Thr Val	Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu					
227		180	185	190			
228							
229	Tyr Leu Ala Phe	Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg					
230		195	200	205			
231							
232	Cys His Phe His	Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu					
233		210	215	220			
234							
235	Gln Ile Tyr Ile	Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu					
236		225	230	235	240		
237							
238	Phe Arg Tyr Ala	Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr					
239		245	250	255			
240							
241	Gly Val Pro Leu	Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr					
242		260	265	270			
243							
244	Leu Gln His Thr	His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp					
245		275	280	285			
246							
247	Asp Trp Phe Arg	Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile					
248		290	295	300			
249							
250	Leu Asn Lys Val	Phe His Asn Ile Thr Asp Thr His Val Ala His His					
251		305	310	315	320		
252							
253	Pro Phe Ser Thr	Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala					
254		325	330	335			
255							
256	Ile Lys Pro Ile	Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val					
257		340	345	350			
258							

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SEQUENCE VERIFICATION REPORT
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Original Text